Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 08:39 PM EDT

PDB ID	:	3OTK
Title	:	Structure and mechanisim of core 2 beta1,6-n-acetylglucosaminyltransferase: a Metal-ion independent gt-a glycosyltransferase
Authors	:	Pak, J.E.; Rini, J.M.
Deposited on	:	2010-09-13
Resolution	:	2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

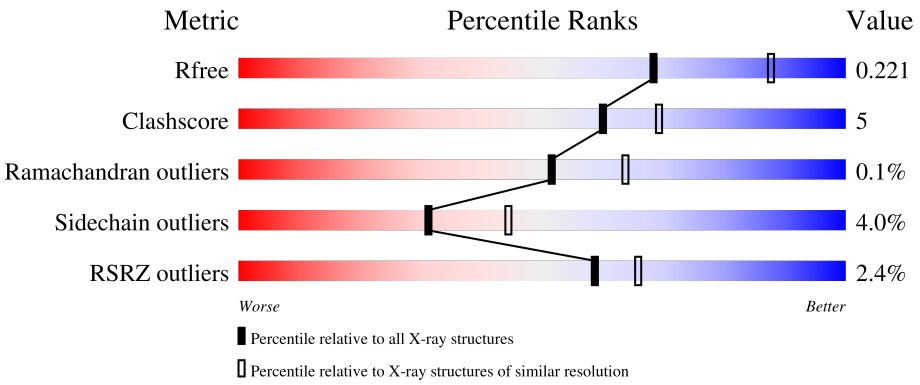
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	391	2%, 81%, 14%, 6%
1	B	391	3%, 80%, 13%, • 7%
1	C	391	3%, 80%, 11%, • 8%
1	D	391	%, 83%, 9%, • 7%
2	E	3	67%, 33%

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Mol	Chain	Length	Quality of chain
2	F	3	67% 33%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 12658 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

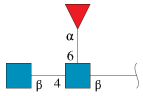
- Molecule 1 is a protein called Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetyl glucosaminyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	369	3015	1936	513	545	21	0	2	0
1	B	363	2956	1897	501	537	21	0	1	0
1	C	360	2934	1881	498	535	20	0	1	0
1	D	364	2966	1905	502	538	21	0	2	0

There are 4 discrepancies between the modelled and reference sequences:

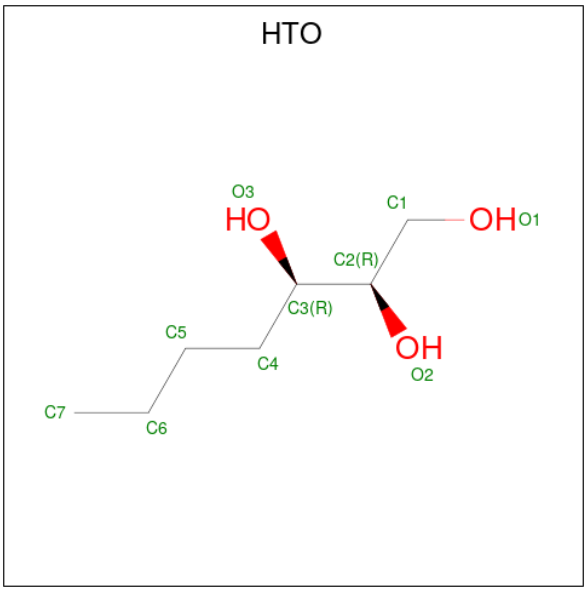
Chain	Residue	Modelled	Actual	Comment	Reference
A	217	SER	CYS	engineered mutation	UNP Q09324
B	217	SER	CYS	engineered mutation	UNP Q09324
C	217	SER	CYS	engineered mutation	UNP Q09324
D	217	SER	CYS	engineered mutation	UNP Q09324

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	3	38	22	2	14	0	0	0
2	F	3	38	22	2	14	0	0	0

- Molecule 3 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula: $C_7H_{16}O_3$).

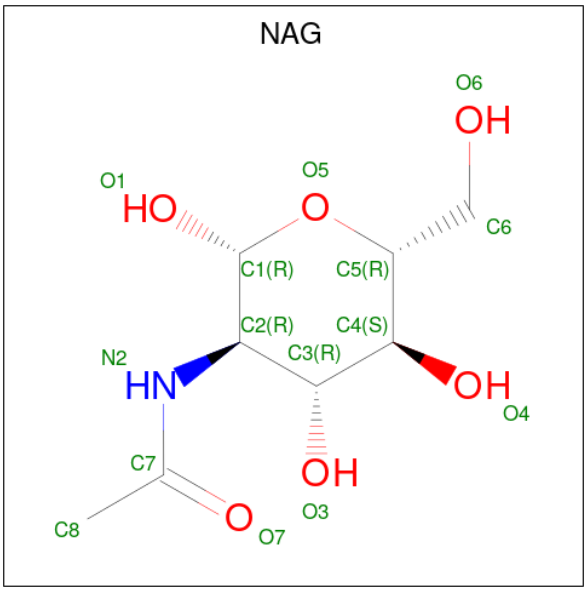


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 10 7 3	0	0
3	A	1	Total C O 10 7 3	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

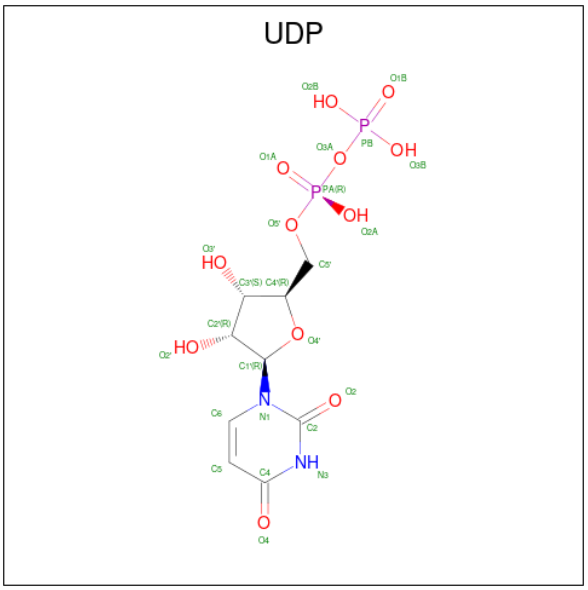
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	14	8	1	5	0	0
			Total	C	N	O		
5	B	1	14	8	1	5	0	0
			Total	C	N	O		
5	C	1	14	8	1	5	0	0
			Total	C	N	O		
5	D	1	14	8	1	5	0	0

- Molecule 6 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: $C_9H_{14}N_2O_{12}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
6	A	1	25	9	2	12	2	0	0
6	B	1	25	9	2	12	2	0	0
6	C	1	25	9	2	12	2	0	0
6	D	1	25	9	2	12	2	0	0

- Molecule 7 is water.

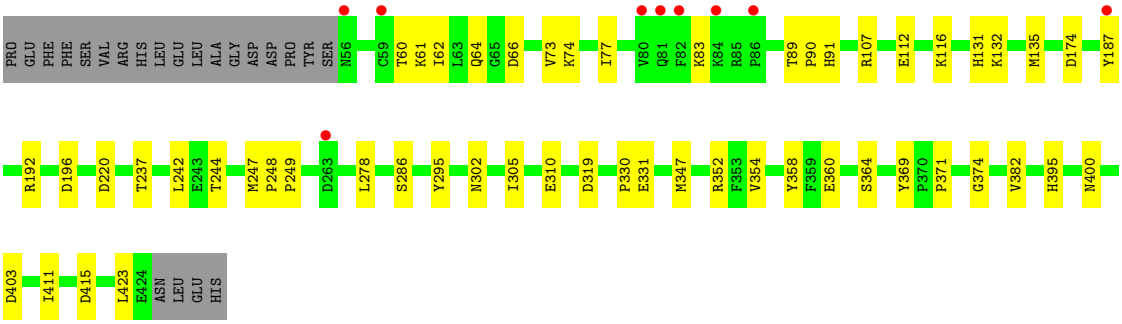
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	143	143	143	0	0
7	B	122	122	122	0	0
7	C	120	120	120	0	0
7	D	148	148	148	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

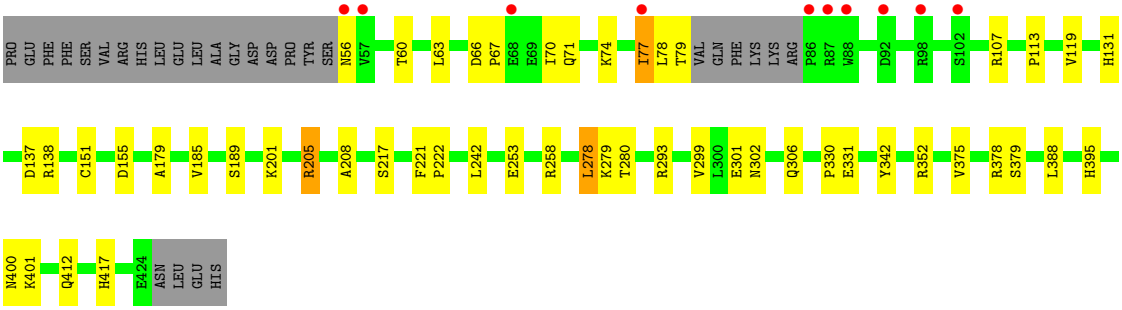
• Molecule 1: Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransfera se

Chain A:



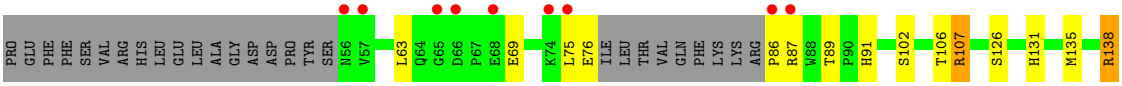
• Molecule 1: Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransfera se

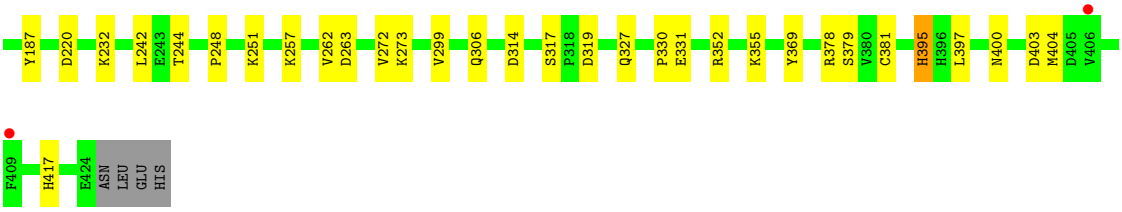
Chain B:



• Molecule 1: Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransfera se

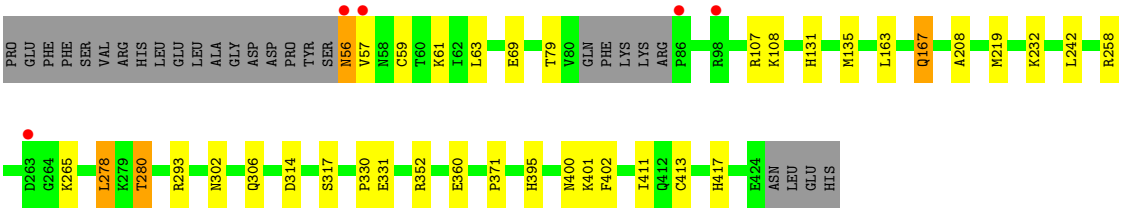
Chain C:





• Molecule 1: Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase

Chain D:



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	73.87Å 101.02Å 136.61Å 90.00° 93.42° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 48.64 – 2.21	Depositor EDS
% Data completeness (in resolution range)	95.4 (50.00-2.30) 93.5 (48.64-2.21)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	1.08 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.165 , 0.219 0.170 , 0.221	Depositor DCC
R_{free} test set	4698 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	25.5	Xtriage
Anisotropy	0.692	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 48.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	12658	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, UDP, NAG, FUC, HTO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.46	0/3096	0.56	0/4197
1	B	0.44	0/3032	0.56	0/4110
1	C	0.44	0/3010	0.57	0/4080
1	D	0.45	0/3048	0.57	0/4132
All	All	0.45	0/12186	0.57	0/16519

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3015	0	2984	32	0
1	B	2956	0	2916	28	0
1	C	2934	0	2881	32	0
1	D	2966	0	2934	20	0
2	E	38	0	34	0	0
2	F	38	0	34	0	0
3	A	20	0	32	4	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	14	0	13	0	0
5	B	14	0	13	0	0
5	C	14	0	13	0	0
5	D	14	0	13	0	0
6	A	25	0	11	2	0
6	B	25	0	11	1	0
6	C	25	0	11	2	0
6	D	25	0	11	0	0
7	A	143	0	0	0	0
7	B	122	0	0	1	0
7	C	120	0	0	1	0
7	D	148	0	0	1	0
All	All	12658	0	11911	110	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (110) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:THR:HG22	1:A:91:HIS:H	1.22	1.04
1:A:89:THR:HG23	1:A:90:PRO:HD2	1.48	0.94
1:C:135:MET:HE2	1:C:404:MET:H	1.43	0.83
1:D:302:ASN:O	1:D:306:GLN:HG2	1.79	0.82
1:C:187:TYR:HE1	6:C:600:UDP:O3B	1.62	0.82
1:A:330:PRO:O	1:A:331:GLU:HB2	1.81	0.79
1:D:163:LEU:O	1:D:167:GLN:HG2	1.87	0.74
1:A:89:THR:HG22	1:A:91:HIS:N	2.00	0.74
1:B:258:ARG:HD3	7:B:439:HOH:O	1.88	0.72
1:B:278:LEU:HD13	1:B:280:THR:O	1.89	0.71
1:C:330:PRO:O	1:C:331:GLU:HB2	1.90	0.71
1:C:220:ASP:OD1	1:C:400:ASN:HB2	1.93	0.69
1:D:61:LYS:CB	1:D:69:GLU:HG3	2.24	0.68
1:B:66:ASP:O	1:B:70:ILE:HG12	1.96	0.65
1:B:138:ARG:HH22	1:B:412:GLN:HG2	1.62	0.65
1:C:63:LEU:HD11	1:C:417:HIS:HB2	1.80	0.64
1:A:89:THR:HG23	1:A:90:PRO:CD	2.25	0.63
1:D:61:LYS:HB2	1:D:69:GLU:HG3	1.82	0.61
1:C:248:PRO:HG2	1:C:251:LYS:HG3	1.83	0.60
1:D:56:ASN:HD22	1:D:57:VAL:N	2.00	0.60
1:C:89:THR:HG23	1:C:91:HIS:H	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:ARG:HH22	1:C:404:MET:CB	2.14	0.60
1:B:201:LYS:O	1:B:205:ARG:HG2	2.02	0.60
1:D:258:ARG:HG3	1:D:314:ASP:OD2	2.03	0.59
1:A:132:LYS:HD3	1:A:135[A]:MET:CE	2.32	0.59
1:B:155:ASP:OD1	1:B:185:VAL:HB	2.03	0.59
1:B:330:PRO:O	1:B:331:GLU:HB2	2.01	0.58
1:A:60:THR:O	1:A:64:GLN:HG3	2.04	0.58
1:D:63:LEU:HD11	1:D:417:HIS:HB2	1.85	0.57
1:C:135:MET:HE2	1:C:404:MET:N	2.17	0.57
1:D:135[A]:MET:CE	1:D:219:MET:HG2	2.35	0.56
1:B:107:ARG:HD3	1:B:137:ASP:OD2	2.06	0.56
1:B:77:ILE:HG22	1:B:78:LEU:N	2.18	0.56
1:C:69:GLU:OE2	1:C:69:GLU:HA	2.04	0.56
1:B:217:SER:HB2	6:B:599:UDP:O3'	2.05	0.55
1:A:220:ASP:OD1	1:A:400:ASN:HB2	2.07	0.55
1:A:364:SER:O	1:B:279:LYS:HE2	2.07	0.54
1:C:135:MET:HE1	1:C:403:ASP:OD1	2.07	0.53
1:D:278:LEU:HD13	1:D:280:THR:O	2.08	0.53
1:B:63:LEU:HD11	1:B:417:HIS:HB2	1.90	0.53
1:C:262:VAL:O	1:C:263:ASP:HB2	2.09	0.53
1:B:71:GLN:HA	1:B:74:LYS:HB2	1.90	0.52
1:A:360:GLU:HB3	1:A:371:PRO:HA	1.92	0.52
1:A:347:MET:HE2	1:B:342:TYR:OH	2.09	0.52
1:D:330:PRO:O	1:D:331:GLU:HB2	2.09	0.51
1:B:302:ASN:O	1:B:306:GLN:HG2	2.10	0.50
1:C:89:THR:HG23	1:C:91:HIS:N	2.27	0.50
1:C:87:ARG:HH22	1:C:404:MET:HB3	1.76	0.50
1:D:258:ARG:HD3	7:D:451:HOH:O	2.12	0.49
1:A:374:GLY:HA3	1:A:382:VAL:O	2.12	0.49
1:A:116:LYS:HG3	3:A:584:HTO:H42	1.94	0.48
1:B:400:ASN:HA	1:B:401:LYS:HA	1.69	0.48
1:D:61:LYS:HB3	1:D:69:GLU:HG3	1.94	0.48
3:A:585:HTO:H3	6:A:598:UDP:O2B	2.14	0.48
1:B:208:ALA:HA	1:B:293:ARG:CZ	2.44	0.48
1:A:89:THR:CG2	1:A:90:PRO:HD2	2.33	0.48
1:C:86:PRO:O	1:C:87:ARG:HD2	2.14	0.47
1:C:327:GLN:HG3	1:C:327:GLN:O	2.14	0.47
1:C:107:ARG:NH1	7:C:508:HOH:O	2.37	0.47
1:D:400:ASN:HA	1:D:401:LYS:HA	1.68	0.47
1:B:378:ARG:O	1:B:379:SER:HB2	2.14	0.46
1:C:63:LEU:CD1	1:C:417:HIS:HB2	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:253:GLU:HA	1:B:253:GLU:OE1	2.17	0.45
1:C:232:LYS:HB3	1:C:232:LYS:HE3	1.82	0.45
1:A:73:VAL:O	1:A:77:ILE:HG12	2.17	0.45
1:A:83:LYS:HE2	1:A:83:LYS:HB3	1.86	0.44
1:A:347:MET:CE	1:B:342:TYR:OH	2.65	0.44
1:C:187:TYR:CE1	6:C:600:UDP:O3B	2.55	0.44
1:A:187:TYR:HE1	6:A:598:UDP:O3B	2.01	0.44
1:C:232:LYS:HD3	1:C:397:LEU:CD2	2.48	0.44
1:A:187:TYR:CE2	3:A:585:HTO:H73	2.52	0.43
1:D:59:CYS:HG	1:D:413:CYS:HG	1.60	0.43
1:A:62:ILE:HD11	1:A:73:VAL:HG21	2.00	0.43
1:B:113:PRO:HB3	1:B:119:VAL:HG23	2.00	0.43
1:B:258:ARG:HE	1:B:258:ARG:HB2	1.67	0.43
1:D:360:GLU:HB3	1:D:371:PRO:HA	2.01	0.43
1:C:102:SER:O	1:C:106:THR:HB	2.18	0.42
1:C:355:LYS:HB2	1:C:381:CYS:HB3	2.01	0.42
1:A:248:PRO:HA	1:A:249:PRO:HD3	1.93	0.42
1:A:411:ILE:O	1:A:415:ASP:HB2	2.20	0.42
1:C:75:LEU:HB2	1:C:76:GLU:H	1.69	0.42
1:A:74:LYS:NZ	1:A:74:LYS:HB3	2.34	0.42
1:D:208:ALA:HA	1:D:293:ARG:CZ	2.49	0.42
1:D:232:LYS:HB3	1:D:232:LYS:HE3	1.85	0.42
1:A:192:ARG:NH1	1:A:196:ASP:OD2	2.47	0.42
1:A:89:THR:CG2	1:A:90:PRO:CD	2.94	0.42
1:C:273:LYS:NZ	1:C:314:ASP:OD1	2.43	0.42
1:A:89:THR:CG2	1:A:90:PRO:N	2.83	0.41
1:A:302:ASN:OD1	1:A:305:ILE:HG12	2.20	0.41
1:B:78:LEU:HD12	1:B:78:LEU:HA	1.95	0.41
1:C:107:ARG:HA	1:C:107:ARG:HE	1.85	0.41
1:C:138:ARG:HE	1:C:404:MET:CE	2.33	0.41
1:B:66:ASP:HA	1:B:67:PRO:HD3	1.92	0.41
1:B:221:PHE:CD2	1:B:222:PRO:HD2	2.56	0.41
1:D:107:ARG:O	1:D:108:LYS:HB2	2.21	0.41
1:B:151:CYS:SG	1:B:179:ALA:HB2	2.61	0.41
1:A:295:TYR:CD2	1:A:295:TYR:C	2.94	0.41
1:C:232:LYS:HE2	1:C:395:HIS:O	2.19	0.41
1:D:265:LYS:HE3	1:D:265:LYS:HB3	1.92	0.41
1:A:61:LYS:HD3	1:A:66:ASP:OD2	2.21	0.41
1:A:135[A]:MET:SD	1:A:403:ASP:HA	2.60	0.41
1:A:247:MET:HA	1:A:248:PRO:HD2	1.96	0.41
1:A:354:VAL:HG22	1:A:400:ASN:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:330:PRO:O	1:B:331:GLU:CB	2.69	0.41
3:A:585:HTO:O2	3:A:585:HTO:H52	2.21	0.41
1:C:257:LYS:HE2	1:C:272:VAL:HG22	2.02	0.40
1:C:87:ARG:HH22	1:C:404:MET:HB2	1.87	0.40
1:D:402:PHE:CB	1:D:411:ILE:HD11	2.51	0.40
1:B:375:VAL:HG12	1:C:75:LEU:HD22	2.02	0.40
1:C:378:ARG:O	1:C:379:SER:HB2	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	369/391 (94%)	359 (97%)	9 (2%)	1 (0%)	41	50
1	B	360/391 (92%)	354 (98%)	6 (2%)	0	100	100
1	C	357/391 (91%)	344 (96%)	13 (4%)	0	100	100
1	D	362/391 (93%)	354 (98%)	8 (2%)	0	100	100
All	All	1448/1564 (93%)	1411 (97%)	36 (2%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	423	LEU

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	333/351 (95%)	318 (96%)	15 (4%)	27	39
1	B	326/351 (93%)	312 (96%)	14 (4%)	29	40
1	C	323/351 (92%)	310 (96%)	13 (4%)	31	44
1	D	328/351 (93%)	318 (97%)	10 (3%)	41	57
All	All	1310/1404 (93%)	1258 (96%)	52 (4%)	31	44

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	ARG
1	A	112	GLU
1	A	131	HIS
1	A	174	ASP
1	A	237	THR
1	A	242	LEU
1	A	244	THR
1	A	278	LEU
1	A	286	SER
1	A	310	GLU
1	A	319	ASP
1	A	352	ARG
1	A	358	TYR
1	A	369	TYR
1	A	395	HIS
1	B	56	ASN
1	B	60	THR
1	B	77	ILE
1	B	79	THR
1	B	131	HIS
1	B	189	SER
1	B	205	ARG
1	B	242	LEU
1	B	278	LEU
1	B	299	VAL
1	B	301	GLU
1	B	352	ARG
1	B	388	LEU
1	B	395	HIS
1	C	107	ARG

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Mol	Chain	Res	Type
1	C	126	SER
1	C	131	HIS
1	C	138	ARG
1	C	242	LEU
1	C	244	THR
1	C	299	VAL
1	C	306	GLN
1	C	317	SER
1	C	319	ASP
1	C	352	ARG
1	C	369	TYR
1	C	395	HIS
1	D	56	ASN
1	D	79	THR
1	D	131	HIS
1	D	167	GLN
1	D	242	LEU
1	D	278	LEU
1	D	280	THR
1	D	317	SER
1	D	352	ARG
1	D	395	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	B	181	GLN
1	B	209	ASN
1	B	313	GLN
1	B	340	ASN
1	B	396	HIS
1	D	56	ASN
1	D	306	GLN
1	D	313	GLN
1	D	340	ASN
1	D	400	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

6 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	E	1	1,2	14,14,15	0.58	0	17,19,21	1.35	1 (5%)
2	NAG	E	2	2	14,14,15	0.54	0	17,19,21	0.65	0
2	FUC	E	3	2	10,10,11	0.64	0	14,14,16	0.69	0
2	NAG	F	1	1,2	14,14,15	0.60	0	17,19,21	1.15	1 (5%)
2	NAG	F	2	2	14,14,15	0.51	0	17,19,21	0.73	0
2	FUC	F	3	2	10,10,11	0.69	0	14,14,16	0.86	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	1/6/23/26	0/1/1/1
2	FUC	E	3	2	-	-	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	FUC	F	3	2	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	1	NAG	C1-O5-C5	4.61	118.36	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	1	NAG	C1-O5-C5	3.86	117.35	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

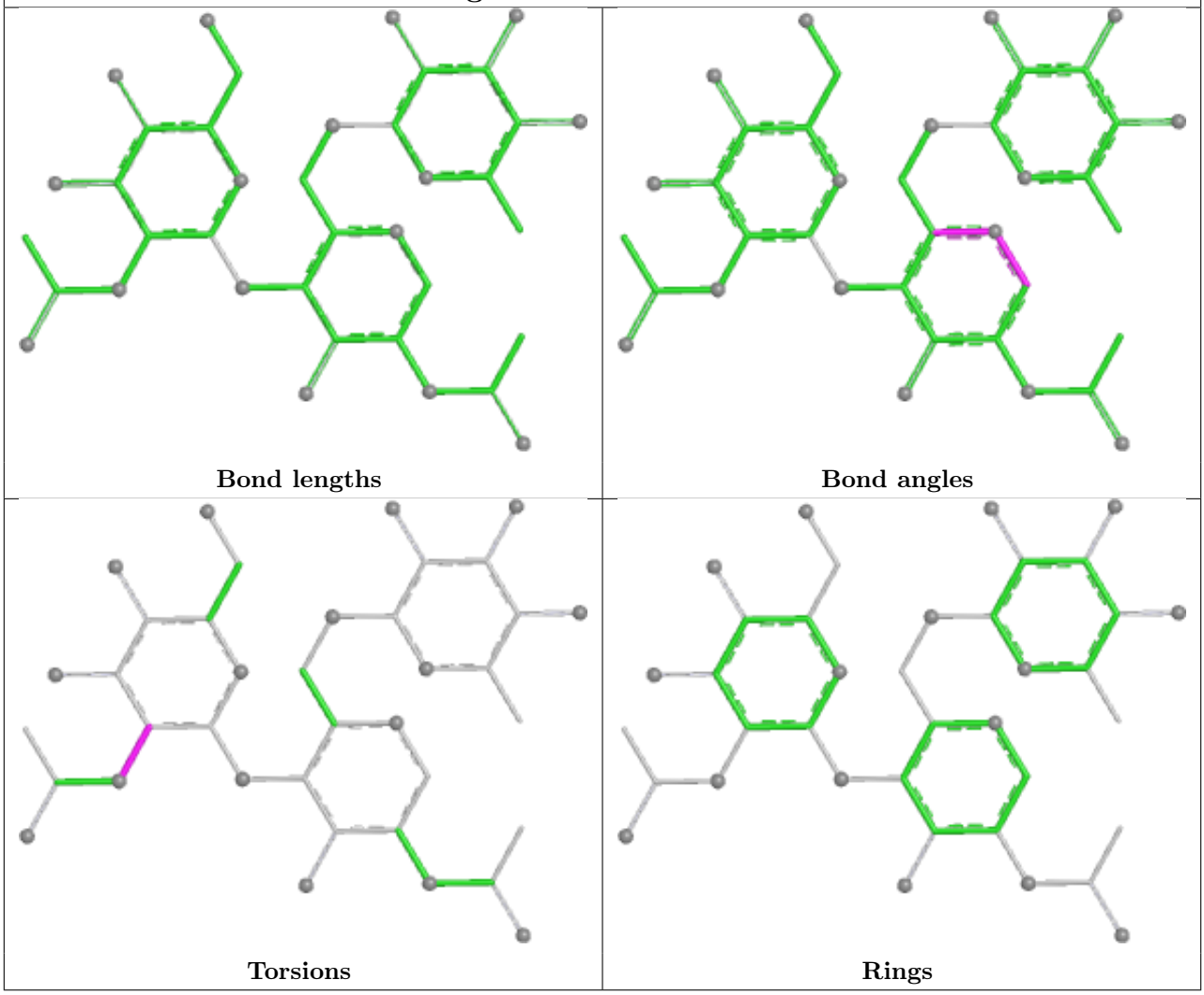
Mol	Chain	Res	Type	Atoms
2	F	2	NAG	O5-C5-C6-O6
2	F	2	NAG	C4-C5-C6-O6
2	E	2	NAG	C1-C2-N2-C7

There are no ring outliers.

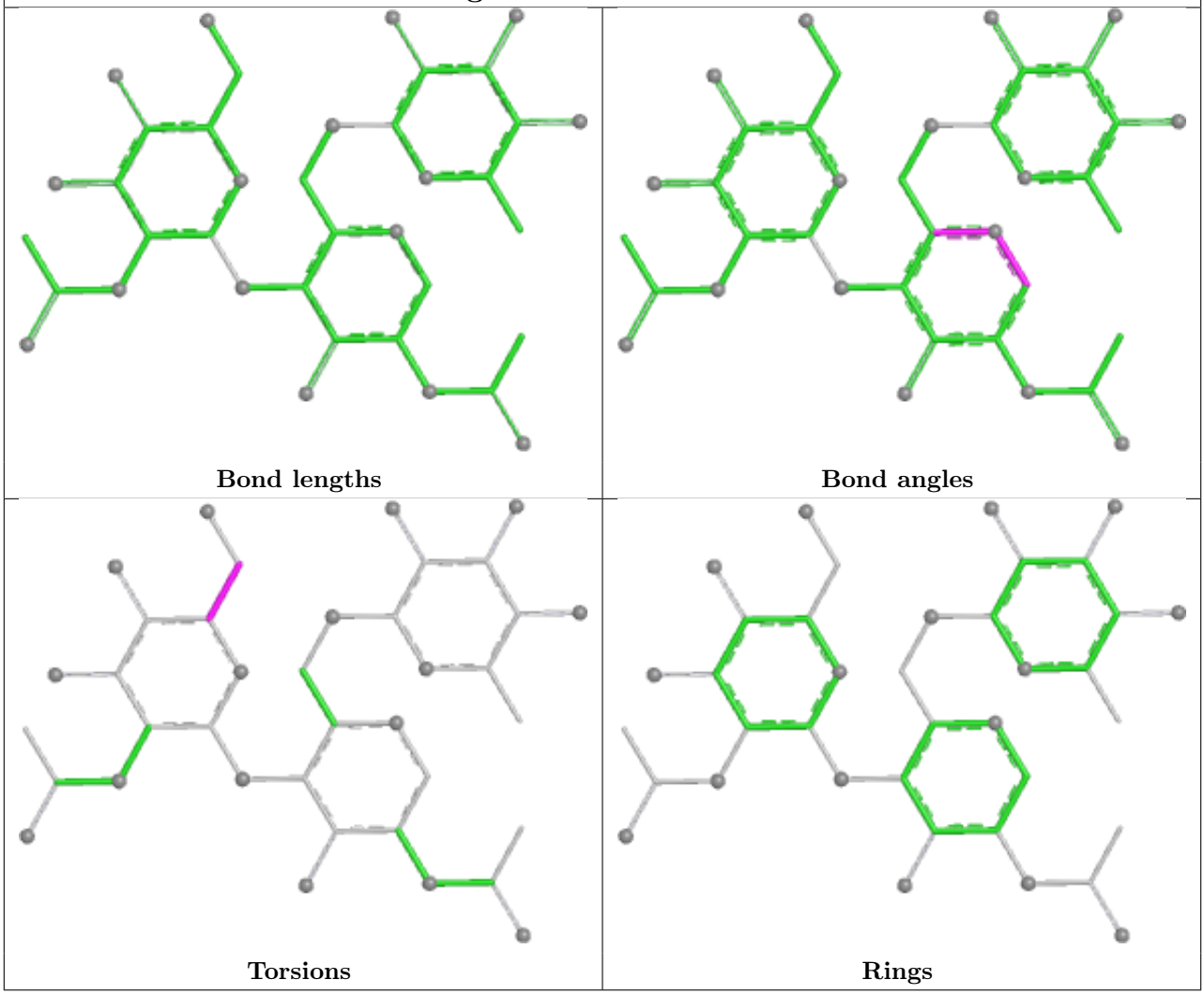
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

Oligosaccharide Chain E



Oligosaccharide Chain F



5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	UDP	A	598	-	25,26,26	0.91	1 (4%)	38,40,40	1.42	5 (13%)
6	UDP	C	600	-	25,26,26	0.99	1 (4%)	38,40,40	1.48	4 (10%)
5	NAG	D	597	1	14,14,15	0.52	0	17,19,21	0.90	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	HTO	A	584	-	9,9,9	0.47	0	10,10,10	0.62	0
6	UDP	D	601	-	25,26,26	1.01	1 (4%)	38,40,40	1.53	5 (13%)
3	HTO	A	585	-	9,9,9	0.38	0	10,10,10	0.77	0
5	NAG	B	592	1	14,14,15	0.47	0	17,19,21	0.79	0
5	NAG	A	588	1	14,14,15	0.50	0	17,19,21	0.92	1 (5%)
5	NAG	C	593	1	14,14,15	0.46	0	17,19,21	0.98	1 (5%)
6	UDP	B	599	-	25,26,26	1.03	2 (8%)	38,40,40	1.58	6 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	UDP	A	598	-	-	2/16/32/32	0/2/2/2
6	UDP	C	600	-	-	2/16/32/32	0/2/2/2
5	NAG	D	597	1	-	2/6/23/26	0/1/1/1
3	HTO	A	584	-	-	7/10/10/10	-
6	UDP	D	601	-	-	6/16/32/32	0/2/2/2
3	HTO	A	585	-	-	1/10/10/10	-
5	NAG	B	592	1	-	4/6/23/26	0/1/1/1
5	NAG	A	588	1	-	0/6/23/26	0/1/1/1
5	NAG	C	593	1	-	0/6/23/26	0/1/1/1
6	UDP	B	599	-	-	4/16/32/32	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	599	UDP	PA-O3A	2.55	1.62	1.59
6	D	601	UDP	C6-C5	2.21	1.40	1.35
6	B	599	UDP	C6-C5	2.06	1.39	1.35
6	A	598	UDP	C6-C5	2.01	1.39	1.35
6	C	600	UDP	PA-O3A	2.01	1.61	1.59

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	599	UDP	C4-N3-C2	-5.35	119.97	126.61
6	C	600	UDP	C4-N3-C2	-5.34	119.98	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	D	601	UDP	C4-N3-C2	-5.30	120.04	126.61
6	A	598	UDP	C4-N3-C2	-4.70	120.77	126.61
6	B	599	UDP	C5-C4-N3	3.91	120.28	114.80
6	C	600	UDP	C5-C4-N3	3.85	120.19	114.80
6	B	599	UDP	N3-C2-N1	3.80	119.84	114.89
6	D	601	UDP	C5-C4-N3	3.79	120.11	114.80
6	D	601	UDP	N3-C2-N1	3.70	119.70	114.89
6	C	600	UDP	N3-C2-N1	3.58	119.55	114.89
6	A	598	UDP	N3-C2-N1	3.50	119.44	114.89
6	A	598	UDP	C5-C4-N3	3.39	119.54	114.80
5	C	593	NAG	C1-O5-C5	3.02	116.24	112.19
6	D	601	UDP	O4-C4-C5	-2.82	120.31	125.16
6	C	600	UDP	O4-C4-C5	-2.55	120.77	125.16
6	B	599	UDP	O4-C4-C5	-2.47	120.89	125.16
6	B	599	UDP	O2-C2-N1	-2.42	119.64	122.80
6	D	601	UDP	O2-C2-N1	-2.40	119.67	122.80
5	A	588	NAG	O5-C5-C6	2.38	112.29	107.66
6	A	598	UDP	O4-C4-C5	-2.06	121.61	125.16
6	B	599	UDP	O4'-C1'-N1	2.04	112.98	108.36
6	A	598	UDP	O4'-C1'-N1	2.01	112.91	108.36

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	584	HTO	C1-C2-C3-O3
3	A	584	HTO	C1-C2-C3-C4
3	A	584	HTO	O2-C2-C3-O3
3	A	584	HTO	O2-C2-C3-C4
5	B	592	NAG	C8-C7-N2-C2
5	B	592	NAG	O7-C7-N2-C2
6	B	599	UDP	C5'-O5'-PA-O1A
6	B	599	UDP	C3'-C4'-C5'-O5'
6	B	599	UDP	O4'-C4'-C5'-O5'
6	D	601	UDP	C3'-C4'-C5'-O5'
6	D	601	UDP	O4'-C4'-C5'-O5'
5	B	592	NAG	C4-C5-C6-O6
5	B	592	NAG	O5-C5-C6-O6
3	A	584	HTO	C4-C5-C6-C7
3	A	584	HTO	C3-C4-C5-C6
3	A	585	HTO	C3-C4-C5-C6
3	A	584	HTO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
6	B	599	UDP	C5'-O5'-PA-O3A
6	D	601	UDP	C5'-O5'-PA-O1A
6	D	601	UDP	C5'-O5'-PA-O2A
6	D	601	UDP	C5'-O5'-PA-O3A
6	A	598	UDP	PA-O3A-PB-O1B
6	A	598	UDP	PA-O3A-PB-O2B
6	C	600	UDP	PA-O3A-PB-O2B
5	D	597	NAG	C8-C7-N2-C2
6	C	600	UDP	PB-O3A-PA-O2A
6	D	601	UDP	C4'-C5'-O5'-PA
5	D	597	NAG	O7-C7-N2-C2

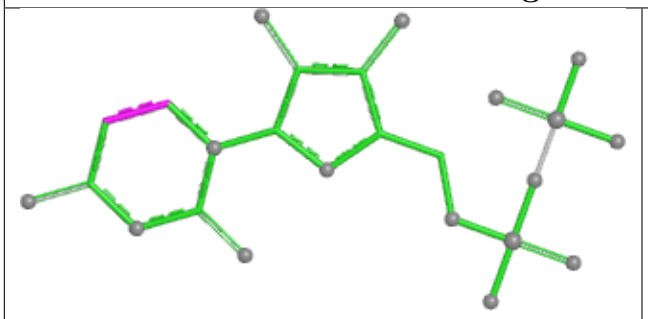
There are no ring outliers.

5 monomers are involved in 8 short contacts:

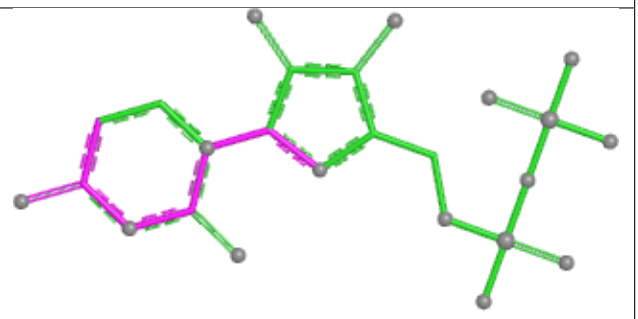
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	598	UDP	2	0
6	C	600	UDP	2	0
3	A	584	HTO	1	0
3	A	585	HTO	3	0
6	B	599	UDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

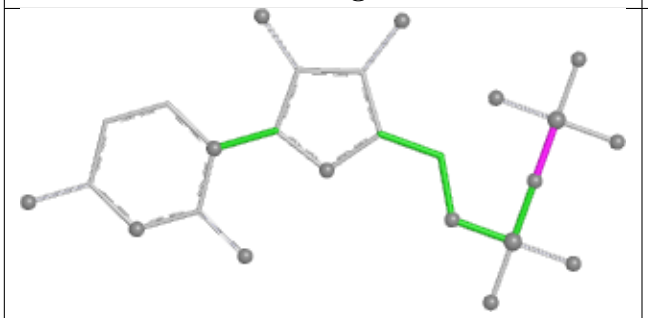
Ligand UDP A 598



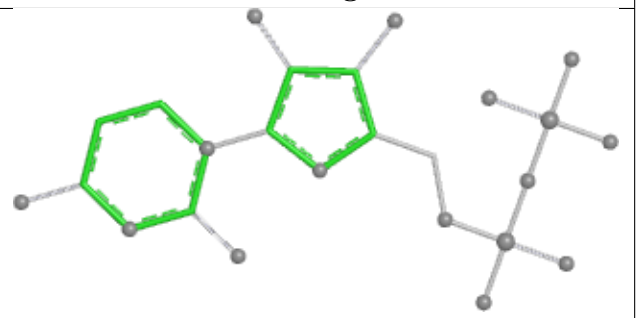
Bond lengths



Bond angles

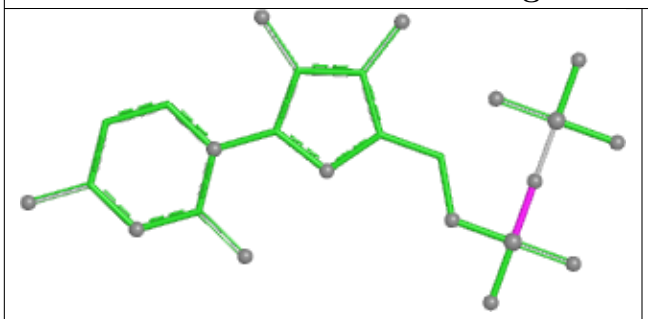


Torsions

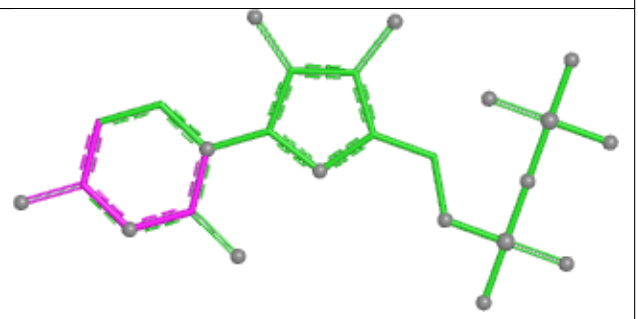


Rings

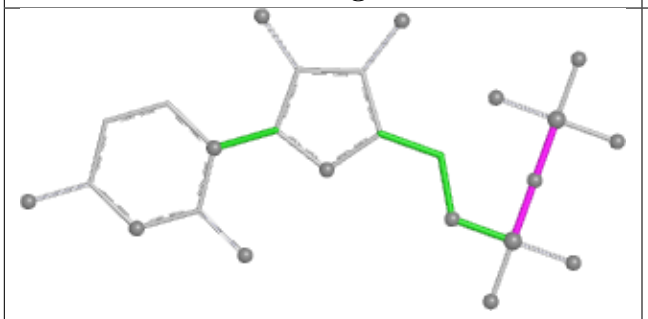
Ligand UDP C 600



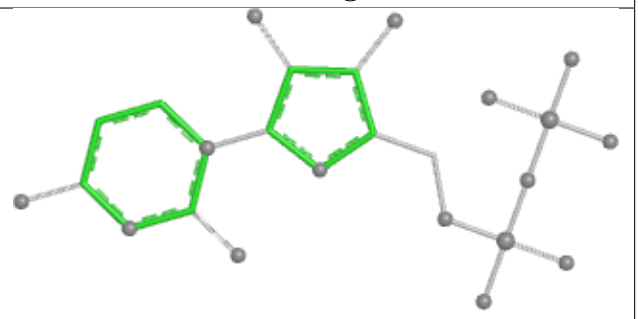
Bond lengths



Bond angles

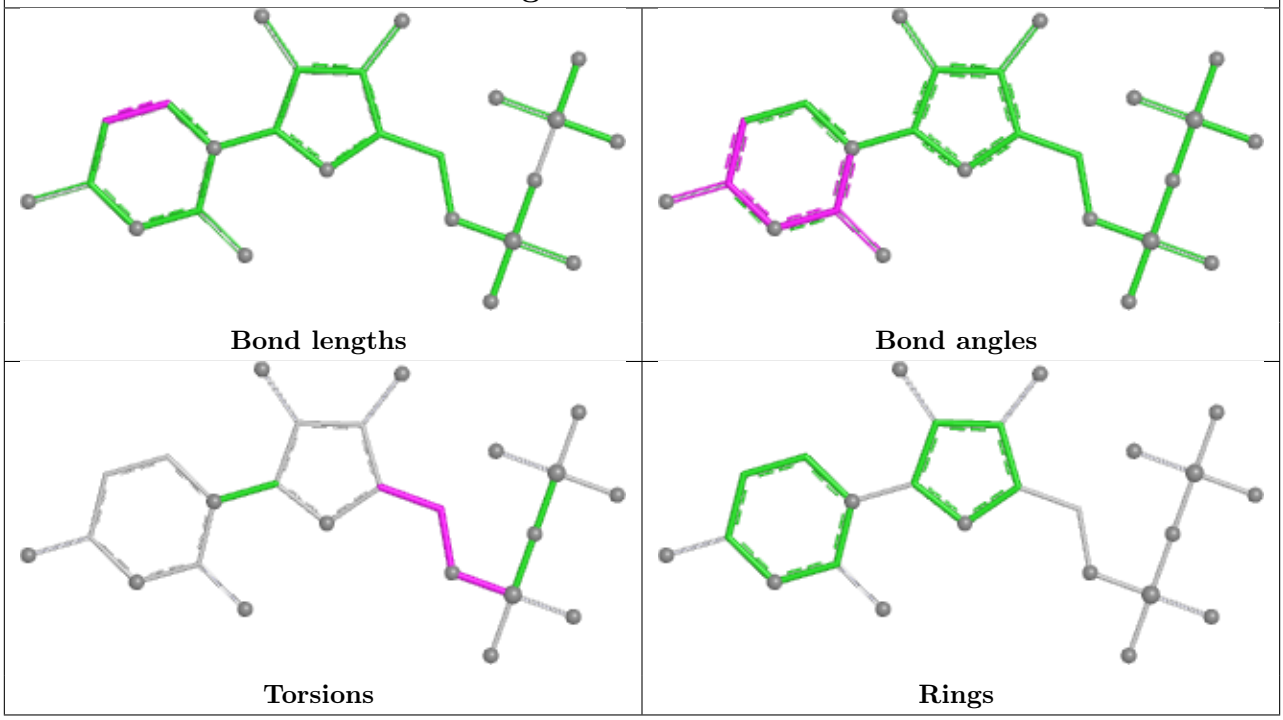


Torsions

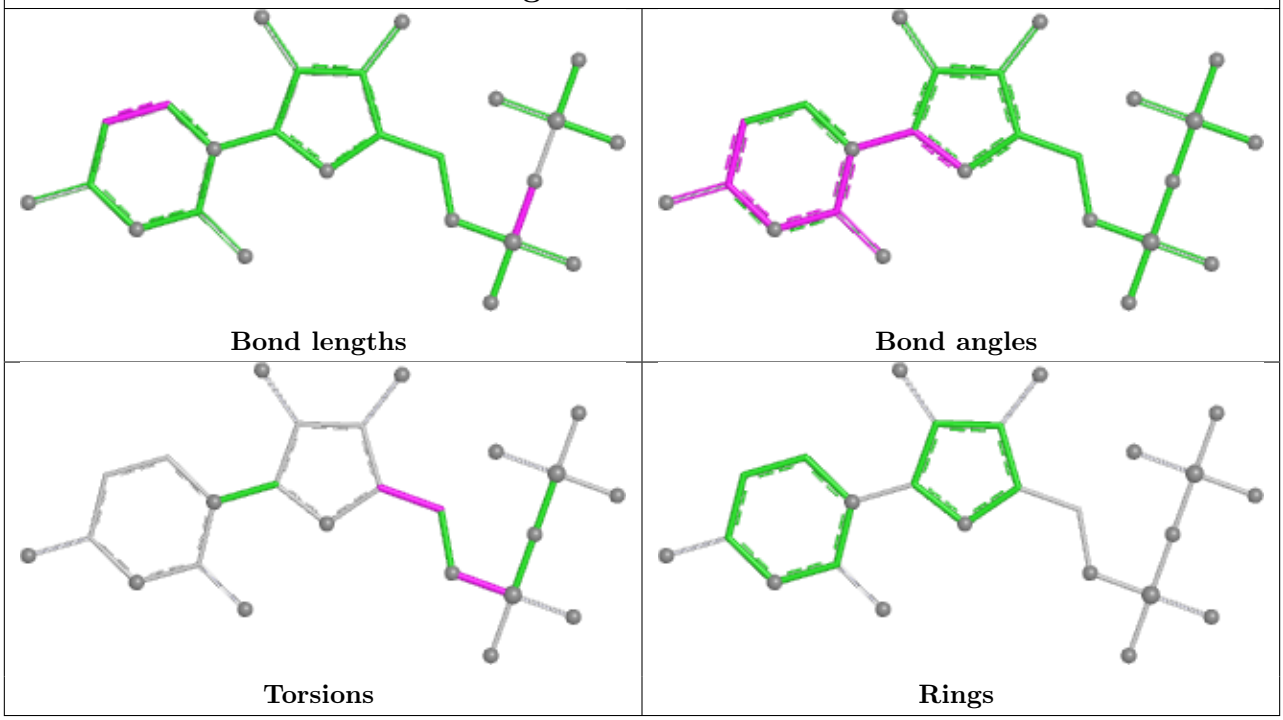


Rings

Ligand UDP D 601



Ligand UDP B 599



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	369/391 (94%)	-0.40	9 (2%)	59	66	23, 38, 66, 96	0
1	B	363/391 (92%)	-0.15	10 (2%)	53	60	24, 42, 76, 103	0
1	C	360/391 (92%)	-0.26	11 (3%)	49	56	22, 39, 73, 95	0
1	D	364/391 (93%)	-0.27	5 (1%)	75	80	22, 39, 63, 88	0
All	All	1456/1564 (93%)	-0.27	35 (2%)	59	66	22, 39, 71, 103	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	86	PRO	5.9
1	C	87	ARG	5.6
1	C	56	ASN	4.9
1	C	86	PRO	4.1
1	B	77	ILE	3.7
1	B	88	TRP	3.4
1	A	80	VAL	3.1
1	B	57	VAL	3.1
1	C	75	LEU	3.1
1	C	68	GLU	3.0
1	A	81	GLN	3.0
1	D	86	PRO	2.8
1	D	57	VAL	2.8
1	B	56	ASN	2.8
1	B	102	SER	2.8
1	A	82	PHE	2.7
1	D	263	ASP	2.6
1	C	409	PHE	2.6
1	C	406	VAL	2.5
1	A	84	LYS	2.5
1	D	56	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	87	ARG	2.5
1	C	57	VAL	2.4
1	B	92	ASP	2.4
1	A	56	ASN	2.3
1	B	98	ARG	2.3
1	A	59	CYS	2.3
1	A	263	ASP	2.2
1	C	66	ASP	2.2
1	A	86	PRO	2.2
1	B	68	GLU	2.2
1	C	65	GLY	2.2
1	C	74	LYS	2.1
1	A	187	TYR	2.1
1	D	98	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

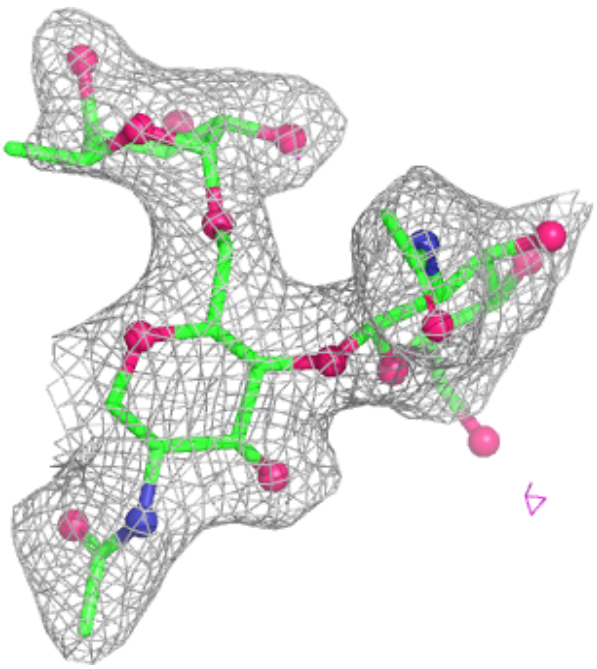
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

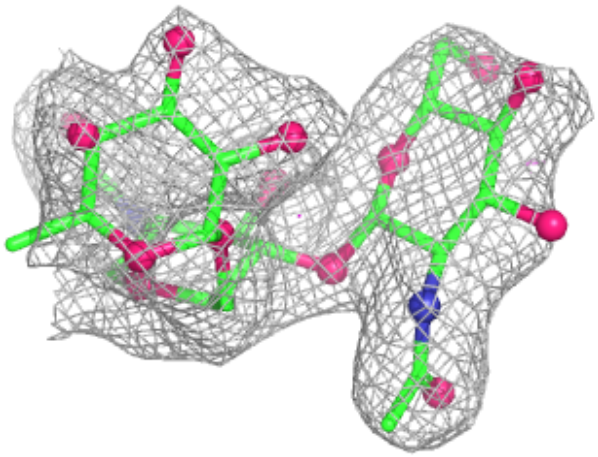
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	F	2	14/15	0.89	0.35	51,91,120,122	0
2	NAG	E	1	14/15	0.93	0.10	38,57,67,67	0
2	FUC	F	3	10/11	0.93	0.26	60,66,79,86	0
2	FUC	E	3	10/11	0.94	0.21	45,68,78,86	0
2	NAG	F	1	14/15	0.94	0.13	37,52,65,70	0
2	NAG	E	2	14/15	0.96	0.18	48,80,98,100	0

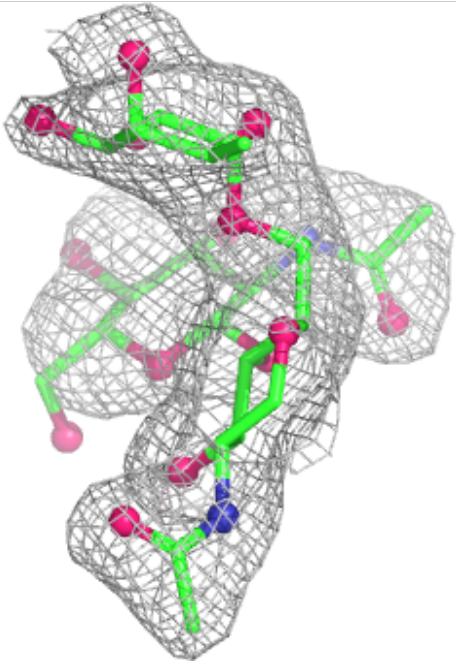
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

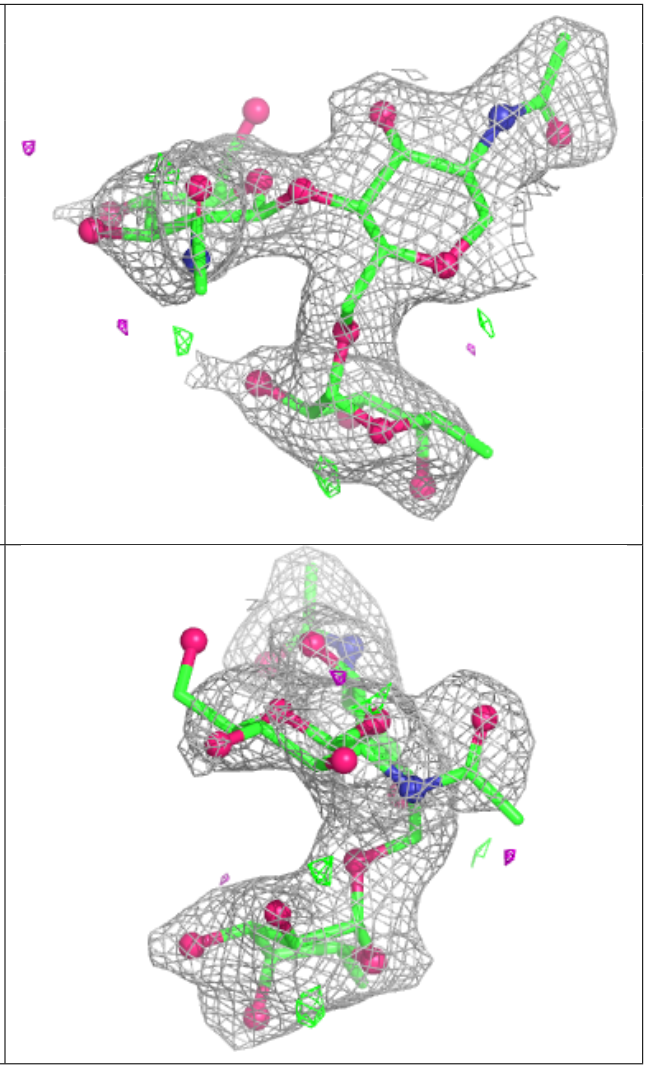






Electron density around Chain F:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	NAG	C	593	14/15	0.65	0.23	75,105,122,129	0
3	HTO	A	584	10/10	0.69	0.26	47,84,110,113	0
5	NAG	D	597	14/15	0.73	0.22	82,105,118,118	0
5	NAG	B	592	14/15	0.74	0.30	94,112,124,125	0
3	HTO	A	585	10/10	0.79	0.19	42,64,75,77	0
4	NA	A	586	1/1	0.82	0.07	43,43,43,43	0
5	NAG	A	588	14/15	0.89	0.20	73,93,107,125	0
6	UDP	B	599	25/25	0.91	0.13	33,63,149,157	0

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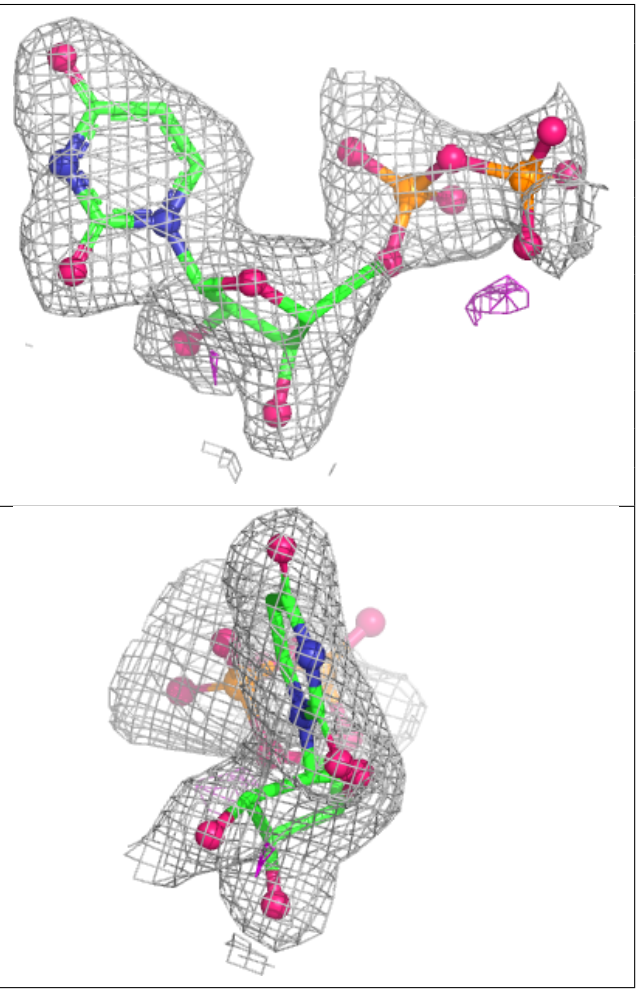
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	UDP	D	601	25/25	0.92	0.12	33,59,142,152	0
6	UDP	C	600	25/25	0.96	0.10	36,53,73,90	0
4	NA	C	587	1/1	0.96	0.08	38,38,38,38	0
6	UDP	A	598	25/25	0.97	0.11	27,40,65,90	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

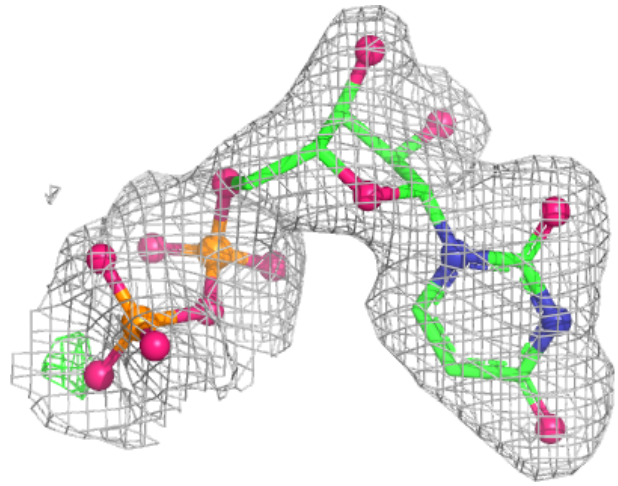
Electron density around UDP B 599:

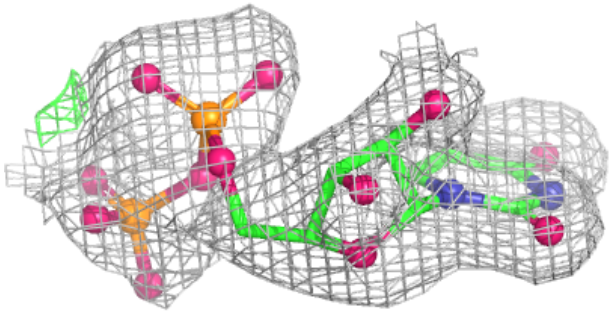
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

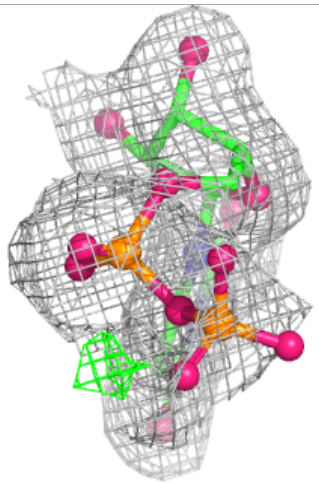


Electron density around UDP D 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

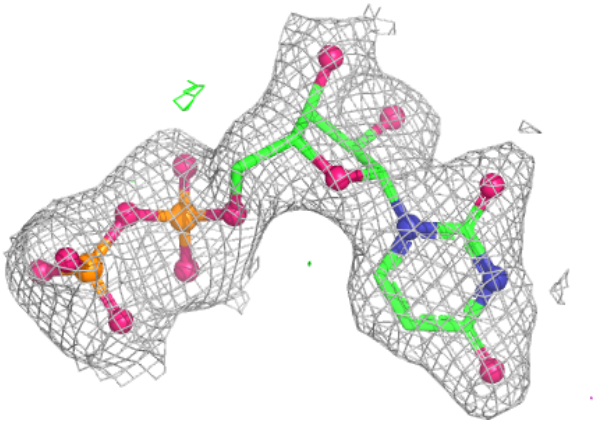


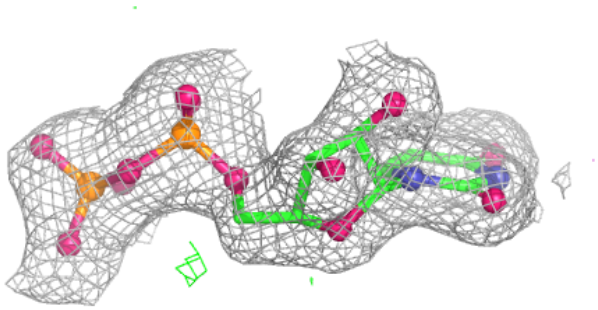


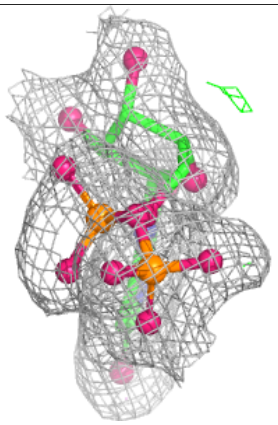


Electron density around UDP C 600:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

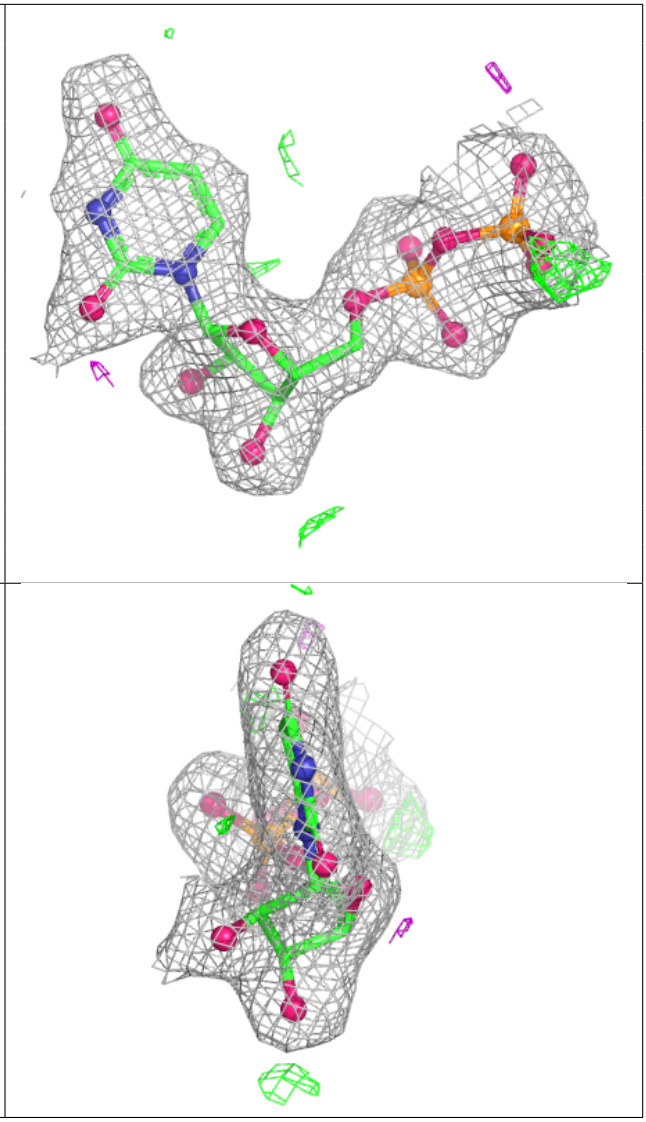






Electron density around UDP A 598:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.